

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 05:11:43 ; Search time 116.57 Seconds

(Without alignments)  
390.303 Million cell updates/sec

Title: US-09-719-748-2\_COPY\_13\_275

Perfect score: 1343  
Sequence: 1 YDIGEELSGGFAIVKCKRE.....LVKERRKRLTIGELRHPWI 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP rvirus: \*  
16: SP bacteriophage: \*  
17: SP archaea: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1332	99.2	370	4	075892	075892 homo sapien
2	1321	98.4	370	4	0901K4	0901K4 homo sapien
3	1297	96.6	370	11	090YMA	090YMA mus musculus
4	1128	84.0	1430	11	090JUP7	090JUP7 mus musculus
5	1125	83.8	345	11	09CV44	09CV44 mus musculus
6	1124	83.7	367	4	09BRL8	09BRL8 homo sapien
7	1121	83.5	454	4	043293	043293 homo sapien
8	1106	82.4	448	11	054784	054784 mus musculus
9	1106	82.4	448	11	088764	088764 rattus norv
10	1073	79.9	303	11	088861	088861 mus musculus
11	745.5	55.5	1435	5	044997	044997 caenorhabdi
12	660.5	49.2	2762	5	P91255	P91255 caenorhabdi
13	646.5	48.1	641	6	09B696	09B696 macaca fasc
14	642.5	47.8	992	4	09C0L5	09C0L5 homo sapien
15	636.5	47.4	907	13	098850	098850 carassius a
16	636	47.4	371	11	091X58	091X58 rattus norv

17	634	47.2	372	11	0923E7	0923E7 mus musculus
18	631.5	47.0	611	11	091XS9	091XS9 cavia porcea
19	627.5	46.7	1721	5	0961U1	0961U1 drosophila
20	627.5	46.7	7107	5	09V4F7	09V4F7 drosophila
21	617.5	46.0	6638	5	076281	076281 drosophila
22	607.5	45.2	451	5	016980	016980 aplysia cal
23	599.5	44.6	795	4	096DV1	096DV1 homo sapien
24	577.5	43.0	1211	5	023260	023260 caenorhabdi
25	576.5	42.9	446	5	095SK9	095SK9 drosophila
26	575	42.8	929	5	001651	001651 drosophila
27	574	42.7	577	5	09GV81	09GV81 drosophila
28	574	42.7	732	5	09GV71	09GV71 drosophila
29	574	42.7	786	5	09GV79	09GV79 drosophila
30	574	42.7	832	5	001653	001653 drosophila
31	574	42.7	913	5	09V7G6	09V7G6 drosophila
32	574	42.7	1289	4	09Y2A5	09Y2A5 homo sapien
33	573	42.7	2959	11	09J1F1	09J1F1 rattus norv
34	569.5	42.4	596	4	09H1R3	09H1R3 homo sapien
35	566	42.1	569	5	001652	001652 drosophila
36	562.5	41.9	6831	5	023550	023550 caenorhabdi
37	562.5	41.9	7160	5	023551	023551 caenorhabdi
38	557.5	41.5	335	5	061269	061269 mytilus gal
39	557.5	41.5	878	5	09GV22	09GV22 mytilus gal
40	541	40.3	4650	4	015598	015598 homo sapien
41	541	40.3	26926	4	010466	010466 homo sapien
42	538	40.1	775	6	097754	097754 cryoclaqus
43	537	40.0	623	5	09GV80	09GV80 drosophila
44	525	39.1	638	5	09VXX9	09VXX9 drosophila
45	521	38.8	980	10	091QR4	091QR4 arabidopsis

## ALIGNMENTS

RESULT 1  
ID 075892 PRELIMINARY; PRT; 370 AA.  
AC 075892;  
DT 01-NOV-1998 (TRMBLrel. 08, Created)  
DT 01-NOV-1998 (TRMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)  
DE DAP-KINASE RELATED PROTEIN 1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY;  
RX MEDLINE=20094983; PubMed=10629061;  
RA "Inbal B., Shani G., Cohen O., Kissil J.L., Kimchi A.,  
RT Serine/Threonine kinase involved in apoptosis.";  
RT Mol. Cell. Biol. 20:1044-1054(2000).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AF052941; AAC35001.1; -  
DR HSSP: Q63450; 1A06.  
DR InterPro: IPR00719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 370 AA; 42923 MW; 09502B4ADC20F91 CRC64;

Query Match 99.2% Score 1332; DB 4; Length 370;  
Best Local Similarity 99.6% Pred. No. 1.5e-95;  
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 YDIGEELSGGFAIVKCKREKSTGLEVAKPIKRRSHRSGVSREREREVILROYL 60

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|||||
Db 23 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKRQSRASRGVSREREVSILRQVL 82
QY 61 HHNVITLHDVYENRTDVVHILEVSGGELFDFLAQKESLSEEAATSFKQLDGVNLT 120
Db 83 HHNVITLHDVYENRTDVVHILEVSGGELFDFLAQKESLSEEAATSFKQLDGVNLT 142
QY 121 KKAIAFDLKPENIMLDKNIPPIHKLIDFGLAHEIEDGVFEKNIFGTPEFAPEIYNYE 180
Db 143 KKAIAFDLKPENIMLDKNIPPIHKLIDFGLAHEIEDGVFEKNIFGTPEFAPEIYNYE 202
QY 181 PLGLEADWMSIGVITYILLSGASPLFGDTKQETLANITSVSYDDEFFSHTSELADFT 240
Db 203 PLGLEADWMSIGVITYILLSGASPLFGDTKQETLANITSVSYDDEFFSHTSELADFT 262
QY 241 RKLIVKETRRKRLTIOEALRHPWI 263
Db 263 RKLIVKETRRKRLTIOEALRHPWI 285

RESULT 2
Q9UIK4 PRELIMINARY; PRT; 370 AA.
ID Q9UIK4
AC Q9UIK4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303018; PubMed=10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akita S.;
RT "Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity."
RL Oncogene 18:3471-3480(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018001; BAA8063.1; -.
DR HSP: Q63450; IAO6.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42898 MW; 035E914BBC881A2 CRC64;
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|||||
QY 181 PLGLEADWMSIGVITYILLSGASPLFGDTKQETLANITSVSYDDEFFSHTSELADFT 240
Db 203 PLGLEADWMSIGVITYILLSGASPLFGDTKQETLANITAVSYDDEFFSHTSELADFT 262
QY 241 RKLIVKETRRKRLTIOEALRHPWI 263
Db 263 RKLIVKETRRKRLTIOEALRHPWI 285

RESULT 3
Q9QYM4 PRELIMINARY; PRT; 370 AA.
ID Q9QYM4
AC Q9QYM4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2 OR DAPK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303018; PubMed=10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akita S.;
RT "Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity."
RL Oncogene 18:3471-3480(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018002; BAA8064.1; -.
DR HSP: Q63450; IAO6.
DR MGD: MGI:1341297; Dapk2.
DR InterPro: IPR000719; Dapk2.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase.1
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42769 MW; 7DA6E29C4DE615B3 CRC64;
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Query Match 96.6%; Score 1297; DB 11; Length 370;  
Best Local Similarity 97.3%; Pred. No. 7,7e-93;  
Matches 256; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKRQSRASRGVSREREVSILRQVL 60
Db 23 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKRQSRASRGVSREREVSILRQVL 82
QY 61 HHNVITLHDVYENRTDVVHILEVSGGELFDFLAQKESLSEEAATSFKQLDGVNLT 120
Db 83 HHNVITLHDVYENRTDVVHILEVSGGELFDFLAQKESLSEEAATSFKQLDGVNLT 142
QY 121 KKAIAFDLKPENIMLDKNIPPIHKLIDFGLAHEIEDGVFEKNIFGTPEFAPEIYNYE 180
Db 143 KKAIAFDLKPENIMLDKNIPPIHKLIDFGLAHEIEDGVFEKNIFGTPEFAPEIYNYE 202
QY 181 PLGLEADWMSIGVITYILLSGASPLFGDTKQETLANITSVSYDDEFFSHTSELADFT 240
Db 203 PLGLEADWMSIGVITYILLSGASPLFGDTKQETLANITAVSYDDEFFSHTSELADFT 262
QY 241 RKLIVKETRRKRLTIOEALRHPWI 263
Db 263 RKLIVKETRRKRLTIOEALRHPWI 285
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RESULT 4
ID 09JUP7 PRELIMINARY: PRT: 1430 AA.
AC 09JUP7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DEATH ASSOCIATED PROTEIN KINASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Klmchl A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: X97048; CAA65762.1; -.
DR HSSP: Q63450; 1A06.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; ank. 8.
DR Pfam: PF00069; pkinase. 1.
DR SMART: SM00248; ANK. 8.
DR SMART: SM00005; DEATH. 1.
DR SMART: SM00220; S_TKC. 1.
DR PROSITE: PS50287; ANK_REPEAT. 7.
DR PROSITE: PS50017; DEATH_DOMAIN. 1.
DR PROSITE: PS50017; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
DR ANK repeat; ATP-binding; Kinase; Repeat;
KM Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 1430 AA; 159843 MW; 81C8356CD14BBE8 CRC64;

Query Match 84.0%; Score 1128; DB 11; Length 1430;
Best Local Similarity 80.2%; Pred. No. 6e-79;
Matches 211; Conservative 37; Mismatches 15; Indels 0; Gaps 0;

OY 1 YDIEEELSGGFAYKKCKREKSTGLEVAAKTIKKRQSNASRGVSRREIEVEVSLKQVL 60
|||
DB 13 YDTEEELSGGFAYKKCKREKSTGLQYAAKFIKKRRKSSRRGVSRREDIEREVSILKEIR 72
OY 61 HHNVITLHDVENRTDVVHILIELVSGELFDFLAKQKESLSREBATSFIKOLLGQVNYLHT 120
|||
DB 73 HPNVITLHEVENKTDVILLIELVAGGELFDFLAKESLREBATEFVKQLLSGVYIHS 132
OY 121 KRIAHFDLKPENIMLDKNIPRIPIKILDFGLAHEIDGVEFKNIFGTPPEVAEIVYE 180
|||
DB 133 LQIAHFDLKPENIMLDKNVPRPKIKIDFGLAKHIDGNEFKNIFGPEVAEIVYE 192
OY 181 PLGLEADWMSIGVITYILLSGASPLDGTKEETLANITSVSYDDEEFFSTSELAKDFI 240
|||
DB 193 PLGLEADWMSIGVITYILLSGASPLDGTKEETLANIVSANVYDDEEFFRNTSTLAKDFI 252
OY 241 RKLIVKETRRKRLTIOEALRHPMI 263
|||
DB 253 RRLIVKDPKKRMTIODSLQHPMI 275

RESULT 5
ID 09CV44 PRELIMINARY: PRT: 345 AA.
AC 09CV44;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

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DE 2310039H24RIK PROTEIN (FRAGMENT).
GN 2310039H24RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009701; BAB26448.1; -.
DR HSSP: Q63450; 1A06.
DR MGD: MGI:1916885; 2310039H24RIK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase. 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKC. 1.
DR SMART: SM00219; TYRK. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR ATP-binding; Transferrase.
KM NON TER
SQ SEQUENCE 345 AA; 39776 MW; FF7D1B4F71CA39C0 CRC64;

Query Match 83.8%; Score 1125; DB 11; Length 345;
Best Local Similarity 79.8%; Pred. No. 1.6e-79;
Matches 210; Conservative 38; Mismatches 15; Indels 0; Gaps 0;

OY 1 YDIEEELSGGFAYKKCKREKSTGLEVAAKTIKKRQSNASRGVSRREIEVEVSLKQVL 60
|||
DB 13 YDTEEELSGGFAYKKCKREKSTGLQYAAKFIKKRRKSSRRGVSRREDIEREVSILKEIR 72
OY 61 HHNVITLHDVENRTDVVHILIELVSGELFDFLAKQKESLSREBATSFIKOLLGQVNYLHT 120
|||
DB 73 HPNVITLHEVENKTDVILLIELVAGGELFDFLAKESLREBATEFVKQLLSGVYIHS 132
OY 121 KRIAHFDLKPENIMLDKNIPRIPIKILDFGLAHEIDGVEFKNIFGTPPEVAEIVYE 180
|||
DB 133 LQIAHFDLKPENIMLDKNVPRPKIKIDFGLAKHIDGNEFKNIFGPEVAEIVYE 192
OY 181 PLGLEADWMSIGVITYILLSGASPLDGTKEETLANITSVSYDDEEFFSTSELAKDFI 240
|||
DB 193 PLGLEADWMSIGVITYILLSGASPLDGTKEETLANIVSANVYDDEEFFRNTSTLAKDFI 252
OY 241 RKLIVKETRRKRLTIOEALRHPMI 263
|||
DB 253 RRLIVKDPKKRMTIODSLQHPMI 275

RESULT 6

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09BTL8  
ID 09BTL8 PRELIMINARY: PRT: 367 AA.  
AC 09BTL8;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE SIMILAR TO DEATH-ASSOCIATED PROTEIN KINASE 1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=MELANOMA;  
RC Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: BC003614; AA03614.1; -  
DR HSSP: 063450; 1A06.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR pfam: PF00069; pkinase.1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00220; S\_TKc; 1.  
DR SMART: SM00219; Tyrc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KM ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 367 AA; 42115 MW; 42EDIDEF191FE3FD CRC64.

Query Match 83.7%; Score 1124; DB 4; Length 367;  
Best Local Similarity 79.5%; Pred. No. 2.1e-79;  
Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

QY 1 YDIGELSGGPAIYKCKREKSTGLEVAKFTKKRSRRGVSREIEREVNLTROVL 60  
DB 13 YDIGELSGGPAIYKCKREKSTGLEVAKFTKKRSRRGVSREIEREVNLTROVL 72  
QY 1 HNNVITLHDVYENRTDVVHILELVSGGELFDLAKESLSEEARSTFKQILDGVNYLT 120  
DB 73 HNNVITLHDVYENRTDVVHILELVSGGELFDLAKESLSEEARSTFKQILDGVNYLT 132  
QY 121 KRIAHDLPENIMLDKNIPRIKIDFGLAHEIDEGVEKNFTGPEFAPEIYVNE 180  
DB 133 LQIAHFDLPENIMLDKNIPRIKIDFGLAHEIDEGVEKNFTGPEFAPEIYVNE 192  
QY 181 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFSSHSELAKDFI 240  
DB 193 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFSSHSELAKDFI 252  
QY 241 RRLVKEETRRKRLTIOEALRHPMI 263  
DB 253 RRLVKEETRRKRLTIOEALRHPMI 275  
RESULT 7  
043293 PRELIMINARY: PRT: 454 AA.  
ID 043293  
AC 043293;  
DT 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 18, Last annotation update)  
DE ZIP-KINASE.  
GN ZIPK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=98147805; PubMed=9488481;  
RA Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;  
RT "ZIP kinase, a novel serine/threonine kinase which mediates  
RT apoptosis";  
RT Mol. Cell. Biol. 18:1642-1651(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9923879; PubMed=10356987;  
RA Murata-Hori M., Suizu F., Iwasaki T., Kikuchi A., Hosoya H.;  
RT "ZIP kinase identified as a novel myosin regulatory light chain kinase  
RT in HeLa cells";  
RT FEBS Lett. 451:81-84(1999).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AB007144; BAA24955.1; -  
DR EMBL: AB022341; BAA81746.1; -  
DR HSSP: 063450; 1A06.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR pfam: PF00069; pkinase.1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KM ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 454 AA; 52535 MW; 56773008A6A61CFC0 CRC64.

Query Match 83.5%; Score 1121; DB 4; Length 454;  
Best Local Similarity 79.8%; Pred. No. 4.7e-79;  
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

QY 1 YDIGELSGGPAIYKCKREKSTGLEVAKFTKKRSRRGVSREIEREVNLTROVL 60  
DB 13 YDIGELSGGPAIYKCKREKSTGLEVAKFTKKRSRRGVSREIEREVNLTROVL 72  
QY 1 HNNVITLHDVYENRTDVVHILELVSGGELFDLAKESLSEEARSTFKQILDGVNYLT 120  
DB 73 HNNVITLHDVYENRTDVVHILELVSGGELFDLAKESLSEEARSTFKQILDGVNYLT 132  
QY 121 KRIAHDLPENIMLDKNIPRIKIDFGLAHEIDEGVEKNFTGPEFAPEIYVNE 180  
DB 133 KRIAHDLPENIMLDKNIPRIKIDFGLAHEIDEGVEKNFTGPEFAPEIYVNE 192  
QY 181 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFSSHSELAKDFI 240  
DB 193 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFSSHSELAKDFI 252  
QY 241 RRLVKEETRRKRLTIOEALRHPMI 263  
DB 253 RRLVKEETRRKRLTIOEALRHPMI 275  
RESULT 8  
054784 PRELIMINARY: PRT: 448 AA.  
ID 054784  
AC 054784;  
DT 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE ZIP-KINASE.  
GN ZIPK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98147805; PubMed=9488481;  
RA Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;  
RT "ZIP kinase, a novel serine/threonine kinase which mediates  
RT apoptosis";  
RT Mol. Cell. Biol. 18:1642-1651(1998).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.







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RESULT 15
ID 098850 PRELIMINARY: PRT; 907 AA.
AC 098850;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NEURONAL MYOSIN LIGHT CHAIN KINASE 1.
GN GFMCLK1.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxId=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COMMON COMET;
RX MEDLINE=97067382; PubMed=8910795;
RA Jian X., Szabo B.G., Schmidt J.T.;
RT "Myosin light chain kinase: expression in neurons and upregulation
RT during axon regeneration.";
RT J. Neurobiol. 31:379-391(1996).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U61731; ABA41402.1; -.
DR HSSP: P56276; ITRK
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; Ig; 2.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00408; IGC2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_UNKNOW_1.
DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Immunoglobulin domain; Kinase;
DR Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 907 AA; 101423 MW; 3B6BA33BF312362C CRC64;

Query Match 47.4%; Score 636.5; DB 13; Length 907;
Best Local Similarity 45.8%; Pred. No. 4.8e-41;
Matches 121; Conservative 56; Mismatches 78; Indels 9; Gaps 3;

QY 1 YDIGELSGGQFAIVKCKGKREKSTGLVAKFTKKRQSRASRGVSRRELEKREVSILROYL 60
DB 470 YDVERRLGTGRGAVFKLEIKSTKVMWAGKFTKAYSAR-----EKDNRQEIATIMDLR 523
QY 61 HHNVITLDHYENRTDVVHILEIVSGGELFDPLAQE-SLSEPEATSFIKOILDGCVNYLH 119
DB 524 HPKLVQCVDAFEGKTDIVMVEWMSGELFERIIDEDELTEREVYIKYIMLDIVDGVSTIH 583
QY 120 TKKIHFDLKPENIMLDKNIPIPIKILIDGLAHEIDGVEEFKNIFGTPFEVAPETVNY 179
DB 584 RKGIVHLDLKPENIMCVNKT--GSKIKLIDGLARLENAGSLKVLFGTPEFVAPETVINY 641
QY 180 EPLGLEADMSIGVITYTLLSGASPELGDTKOETLANITSVSDPDEFESHTSELADF 239
DB 642 EALSTADMSIGVICYLVLSGLSPMGDNDNETLSTVNTSATWDFEAFDEISDEAKDF 701
QY 240 IRKLLVETRRRLTIQELARHPWI 263
DB 702 ISNLLKDKMARLSGDQCFQHPWL 725
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